

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

OCR-754.CIP

Applicants	James M. Anderson and Christina M. Van Itallie
Serial No. - pending	Filing Date: June 25, 2001
Art Unit 1644	Examiner Patrick Nolan
Title of Application	Human Occludin, Its Uses and Enhancement of Drug Absorption Using Occludin Inhibitors

Commissioner of Patents
and Trademarks
Washington, DC 20231

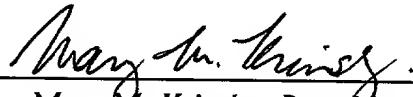
SUBMISSION OF A SEQUENCE STATEMENT UNDER 37 C.F.R. § 1.821(g)

Dear Sir:

The computer-readable form submitted herewith with an application that is a C.I.P. of U.S. application serial number 09/142,732, filed September 15, 1998, is identical to the Sequence Listing of its parent case and that filed in the international parent case, PCT/US97/05809, filed March 14, 1997, and contains no new matter.

Respectfully submitted,

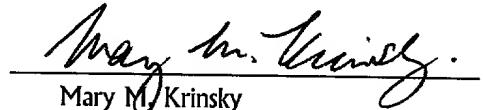
June 25, 2001 by



Mary M. Krinsky, Reg. No. 32423
79 Trumbull Street
New Haven, CT 06511-3708
(203) 773-9544

I hereby certify that this paper and the application are today being deposited with the United States Postal Service as Express Mail, no. EL572277375US, under 37 C.F.R. § 1.10 in an envelope addressed to the Box New Application, Commissioner of Patents, Washington, D.C. 20231.

June 25, 2001


Mary M. Krinsky

1/7
SEQUENCE LISTING

(1) GENERAL INFORMATION

- (i) APPLICANTS: James M. Anderson
Christina M. Van Itallie
- (ii) TITLE OF INVENTION: Human Occludin, Its Uses
and Enhancement of Drug Absorption Using Occludin Inhibitors
- (iii) NUMBER OF SEQUENCES: 6

(iv) CORRESPONDENCE ADDRESS

- (A) ADDRESSEE: Yale University Medical School
Section of Pulmonary and Critical Care Medicine
Department of Internal Medicine
- (B) STREET: 333 Cedar Street, LCI 105
- (C) CITY: New Haven
- (D) STATE: Connecticut
- (E) COUNTRY: United States of America
- (F) ZIP CODE: 065220-8057

(v) COMPUTER READABLE FORM

- (A) MEDIUM TYPE: 3.5" 1.44 Mb diskette
- (B) COMPUTER: IBM PC
- (C) OPERATING SYSTEM: MS DOS
- (D) SOFTWARE: Word Processing

(vi) CURRENT APPLICATION DATA

- (A) APPLICATION NUMBER:
- (B) FILING DATE: June 25, 2001
- (C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA

- (A) APPLICATION NUMBER: U.S. 09/142,732
- (B) FILING DATE: September 15, 1998
- (C) CLASSIFICATION: 530-350.000

(viii) ATTORNEY INFORMATION

- (A) NAME: Mary M. Krinsky
- (B) REGISTRATION NO.: 32423
- (C) REFERENCE/DOCKET NUMBER: OCR-754.CIP

(ix) TELECOMMUNICATION INFORMATION

- (A) TELEPHONE NUMBER: 203-773-9544
- (B) TELEFAX NUMBER: 203-773-1183

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2312
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE:

- (A) DESCRIPTION: cDNA

(v) FRAGMENT TYPE: complete sequence

(ix) FEATURE:

- (A) NAME/KEY: human occludin

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

GCCTCTCTCC	ATCAGACACC	CCAAGGTTCC	ATCCGAAGCA	GGCGGAGCAC	50
CGAACGCACC	CCGGGGTGGT	CAGGGACCCC	CATCCGTGCT	GCCCCCTAGG	100
AGCCCGCGCC	TCTCCTCTGC	GCCCCGCCTC	TCGGGCCGCA	ACATCGCGCG	150
GTTCCTTAA	CAGCGCGCTG	GCAGGGTGTG	GGAAGCAGGA	CCGCGTCCTC	200
CCGCCCCCTC	CCATCCGAGT	TTCAGGTGAA	TTGGTCACCG	AGGGAGGAGG	250
CCGACACACC	ACACCTACAC	TCCCGCGTCC	ACCTCTCCCT	CCCTGCTTCC	300
TCTTGGCGGA	GGCGGCAGGA	ACCGAGAGCC	AGGTCCAGAG	CGCCGAGGAG	350
CCGGTCTAGG	ACGCAGCAGA	TTGGTTTATC	TTGGAAGCTA	AAGGGCATTG	400
CTCATCCTGA	AGATCAGCTG	ACCATTGACA	ATCAGCCATG	TCATCCAGGC	450
CTCTTGAAAG	TCCACCTCCT	TACAGGCCTG	ATGAATTCAA	ACCGAATCAT	500
TATGCACCAA	GCAATGACAT	ATATGGTGGA	GAGATGCATG	TTCGACCAAT	550
GCTCTCTCAG	CCAGCCTACT	CTTTTACCC	AGAAGATGAA	ATTCTTCACT	600
TCTACAAATG	GACCTCTCCT	CCAGGAGTGA	TTCGGATCCT	GTCTATGCTC	650
ATTATTGTGA	TGTGCATTGC	CATCTTGCC	TGTGTGGCCT	CCACGCTTGC	700
CTGGGACAGA	GGCTATGGAA	CTTCCCTTTT	AGGAGGTAGT	GTAGGCTACC	750
CTTATGGAGG	AAGTGGCTTT	GGTAGCTACG	GAAGTGGCTA	TGGCTATGGC	800
TATGGTTATG	GCTATGGCTA	CGGAGGCTAT	ACAGACCCAA	GAGCAGCAAA	850
GGGCTTCATG	TTGGCCATGG	CTGCCTTTG	TTTCATTGCC	GCGTTGGTGA	900
TCTTTGTTAC	CAGTGTATATA	AGATCTGAAA	TGTCCAGAAC	AAGAAGATAC	950
TACTTAAGTG	TGATAATAGT	GAGTGCTATC	CTGGGCATCA	TGGTGTATTAT	1000
TGCCACAATT	GTCTATATAA	TGGGAGTGA	CCCAACTGCT	CAGTCTTCTG	1050
GATCTCTATA	TGGTTCACAA	ATATATGCC	TCTGCAACCA	ATTTTATACA	1100
CCTGCAGCTA	CTGGACTCTA	CGTGGATCAG	TATTTGTATC	ACTACTGTGT	1150
TGTGGATCCC	CAGGAGGCCA	TTGCCATTGT	ACTGGGGTTC	ATGATTATTG	1200

TGGCTTTGC TTTAATAATT TTCTTTGCTG TGAAAACCTCG AAGAAAGATG 1250
 GACAGGTATG ACAAGTCCAA TATTTGTGG GACAAGGAAC ACATTTATGA 1300
 TGAGCAGCCC CCCAATGTCG AGGAGTGGGT TAAAAATGTG TCTGCAGGCA 1350
 CACAGGACGT GCCTTCACCC CCATCTGACT ATGTGGAAAG AGTTGACAGT 1400
 CCCATGGCAT ACTCTTCCAA TGGCAAAGTG AATGACAAGC GGTTTTATCC 1450
 AGAGTCTTCC TATAAATCCA CGCCGGTTCC TGAAGTGGTT CAGGAGCTTC 1500
 CATTAACCTTC GCCTGTGGAT GACTTCAGGC AGCCTCGTTA CAGCAGCGGT 1550
 GGTAACTTG AGACACCTTC AAAAAGAGCA CCTGCAAAGG GAAGAGCAGG 1600
 AAGGTCAAAG AGAACAGAGC AAGATCACTA TGAGACAGAC TACACAAC TG 1650
 GCGGCGAGTC CTGTGATGAG CTGGAGGAGG ACTGGATCAG GGAATATCCA 1700
 CCTATCACTT CAGATCAACA AAGACAAC TG TACAAGAGGA ATTTGACAC 1750
 TGGCCTACAG GAATACAAGA GCTTACAATC AGAACTTGAT GAGATCAATA 1800
 AAGAACTCTC CCGTTGGAT AAAGAATTGG ATGACTATAG AGAAGAAAGT 1850
 GAAGAGTACA TGGCTGCTGC TGATGAATAC AATAGACTGA AGCAAGTGAA 1900
 GGGATCTGCA GATTACAAAA GTAAGAAGAA TCATTGCAAG CAGTTAAAGA 1950
 GCAAATTGTC ACACATCAAG AAGATGGTTG GAGACTATGA TAGACAGAAA 2000
 ACATAGAAGG CTGATGCCAA GTTGTGAG AAATTAAGTA TCTGACATCT 2050
 CTGCAATCTT CTCAGAAGGC AAATGACTTT GGACCATAAC CCCGGAAGGCC 2100
 AACACCTCTGT GAGCATCACA AAGTTTGAG TTGCTTTAAC ATCATCAGTA 2150
 TTGAAGCATT TTATAAATCG CTTTGATAA TCAACTGGGC TGAACAACTC 2200
 CAATTAAGGA TTTTATGCTT TAAACATTGG TTCTTGTATT AAGAATGAAA 2250
 TACTGTTGA GGTTTTAACG CCTTAAAGGA AGGTTCTGGT GTGAACACTAA 2300
 CTTTCACACC CC 2312

(3) INFORMATION FOR SEQ ID NO: 2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 522
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE:
 - (A) DESCRIPTION: polypeptide
- (v) FRAGMENT TYPE: complete sequence
- (ix) FEATURE:
 - (A) NAME/KEY: human occludin

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Met	Ser	Ser	Arg	Pro	Leu	Glu	Ser	Pro	Pro	Pro	Tyr	Arg	Pro	Asp	5	10	15
Glu	Phe	Lys	Pro	Asn	His	Tyr	Ala	Pro	Ser	Asn	Asp	Ile	Tyr	Gly	20	25	30
Gly	Glu	Met	His	Val	Arg	Pro	Met	Leu	Ser	Gln	Pro	Ala	Tyr	Ser	35	40	45
Phe	Tyr	Pro	Glu	Asp	Glu	Ile	Leu	His	Phe	Tyr	Lys	Trp	Thr	Ser	50	55	60
Pro	Pro	Gly	Val	Ile	Arg	Ile	Leu	Ser	Met	Leu	Ile	Ile	Val	Met	65	70	75
Cys	Ile	Ala	Ile	Phe	Ala	Cys	Val	Ala	Ser	Thr	Leu	Ala	Trp	Asp	80	85	90
Arg	Gly	Tyr	Gly	Thr	Ser	Leu	Leu	Gly	Gly	Ser	Val	Gly	Tyr	Pro	95	100	105
Tyr	Gly	Gly	Ser	Gly	Phe	Gly	Ser	Tyr	Gly	Ser	Gly	Tyr	Gly	Tyr	110	115	120
Gly	Tyr	Gly	Tyr	Gly	Tyr	Gly	Tyr	Gly	Gly	Tyr	Thr	Asp	Pro	Arg	125	130	135
Ala	Ala	Lys	Gly	Phe	Met	Leu	Ala	Met	Ala	Ala	Phe	Cys	Phe	Ile	140	145	150
Ala	Ala	Leu	Val	Ile	Phe	Val	Thr	Ser	Val	Ile	Arg	Ser	Glu	Met	155	160	165
Ser	Arg	Thr	Arg	Arg	Tyr	Tyr	Leu	Ser	Val	Ile	Ile	Val	Ser	Ala	170	175	180
Ile	Leu	Gly	Ile	Met	Val	Phe	Ile	Ala	Thr	Ile	Val	Tyr	Ile	Met	185	190	195
Gly	Val	Asn	Pro	Thr	Ala	Gln	Ser	Ser	Gly	Ser	Leu	Tyr	Gly	Ser	200	205	210
Gln	Ile	Tyr	Ala	Leu	Cys	Asn	Gln	Phe	Tyr	Thr	Pro	Ala	Ala	Thr	215	220	225
Gly	Leu	Tyr	Val	Asp	Gln	Tyr	Leu	Tyr	His	Tyr	Cys	Val	Val	Asp	230	235	240
Pro	Gln	Glu	Ala	Ile	Ala	Ile	Val	Leu	Gly	Phe	Met	Ile	Ile	Val	245	250	255

Ala Phe Ala Leu Ile Ile Phe Phe Ala Val Lys Thr Arg Arg Lys
 260 265 270
 Met Asp Arg Tyr Asp Lys Ser Asn Ile Leu Trp Asp Lys Glu His
 275 280 285
 Ile Tyr Asp Glu Gln Pro Pro Asn Val Glu Glu Trp Val Lys Asn
 290 295 300
 Val Ser Ala Gly Thr Gln Asp Val Pro Ser Pro Pro Ser Asp Tyr
 305 310 315
 Val Glu Arg Val Asp Ser Pro Met Ala Tyr Ser Ser Asn Gly Lys
 320 325 330
 Val Asn Asp Lys Arg Phe Tyr Pro Glu Ser Ser Tyr Lys Ser Thr
 335 340 345
 Pro Val Pro Glu Val Val Gln Glu Leu Pro Leu Thr Ser Pro Val
 350 355 360
 Asp Asp Phe Arg Gln Pro Arg Tyr Ser Ser Gly Gly Asn Phe Glu
 365 370 375
 Thr Pro Ser Lys Arg Ala Pro Ala Lys Gly Arg Ala Gly Arg Ser
 380 385 390
 Lys Arg Thr Glu Gln Asp His Tyr Glu Thr Asp Tyr Thr Thr Gly
 395 400 405
 Gly Glu Ser Cys Asp Glu Leu Glu Glu Asp Trp Ile Arg Glu Tyr
 410 415 420
 Pro Pro Ile Thr Ser Asp Gln Gln Arg Gln Leu Tyr Lys Arg Asn
 425 430 435
 Phe Asp Thr Gly Leu Gln Glu Tyr Lys Ser Leu Gln Ser Glu Leu
 440 445 450
 Asp Glu Ile Asn Lys Glu Leu Ser Arg Leu Asp Lys Glu Leu Asp
 455 460 465
 Asp Tyr Arg Glu Glu Ser Glu Glu Tyr Met Ala Ala Ala Asp Glu
 470 475 480
 Tyr Asn Arg Leu Lys Gln Val Lys Gly Ser Ala Asp Tyr Lys Ser
 485 490 495
 Lys Lys Asn His Cys Lys Gln Leu Lys Ser Lys Leu Ser His Ile
 500 505 510
 Lys Lys Met Val Gly Asp Tyr Asp Arg Gln Lys Thr
 515 520

(4) INFORMATION FOR SEQ ID NO: 3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE:
 - (A) DESCRIPTION: peptide
- (v) FRAGMENT TYPE: synthetic peptide
- (ix) FEATURE:
 - (D) OTHER INFORMATION: construct used in experiments
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

Cys Asp Arg Gly Tyr Gly Thr Ser Leu Leu Gly Gly Ser Val Gly
5 10 15

Tyr Pro Tyr Gly Gly Ser Gly Phe Gly
20

(5) INFORMATION FOR SEQ ID NO: 4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE:
 - (A) DESCRIPTION: peptide
- (v) FRAGMENT TYPE: synthetic peptide
- (ix) FEATURE:
 - (D) OTHER INFORMATION: construct used in experiments
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Cys Ser Tyr Gly Ser Gly Tyr Gly Tyr Gly Tyr Gly Tyr Gly Tyr
5 10 15

Gly Tyr Gly Gly Tyr Thr Asp Pro Arg
20

(6) INFORMATION FOR SEQ ID NO: 5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE:
 - (A) DESCRIPTION: peptide
- (v) FRAGMENT TYPE: synthetic peptide
- (ix) FEATURE:
 - (D) OTHER INFORMATION: construct used in experiments
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

Asn His Tyr Ala Pro Ser Asn Asp Ile Tyr Gly Gly Glu Met Val
5 10 15

His Arg Pro Met Leu
20

(7) INFORMATION FOR SEQ ID NO: 6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 11
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE:
 - (A) DESCRIPTION: peptide
- (v) FRAGMENT TYPE: synthetic peptide
- (ix) FEATURE:
 - (D) OTHER INFORMATION: construct used in experiments
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Ala Ser Gln Gln Val Tyr Arg Lys Asp Pro Cys
5 10